

Gencore version 5.1.7
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OM protein - protein search, using bw model.

Run on: February 4, 2006, 13:58:25 ; Search time 16 Seconds

(without alignments)

623.987 Million cell updates/sec

Perfect score: 4331

Sequence: 1 MSSVPIQPSRLPLLTHR.....AAPDGFTVKTRPGILNSKL 852

Scoring table: BLOSUM62

Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters:

88029

Minimum DB seq length: 0

Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New.*

1: /cgm2_6/ptodata/2/pubpa/US08_NEW_PUB.PEP.*

2: /cgm2_6/ptodata/2/pubpa/US06_NEW_PUB.PEP.*

3: /cgm2_6/ptodata/2/pubpa/PCP_NEW_PUB.PEP.*

4: /cgm2_6/ptodata/2/pubpa/PCP_NEW_PUB.PEP.*

5: /cgm2_6/ptodata/2/pubpa/US05_NEW_PUB.PEP.*

6: /cgm2_6/ptodata/2/pubpa/US04_NEW_PUB.PEP.*

7: /cgm2_6/ptodata/2/pubpa/US11_NEW_PUB.PEP.*

8: /cgm2_6/ptodata/2/pubpa/US60_NEW_PUB.PEP.*

ALIGNMENTS

RESULT 1
 US-10-467-657-4910/ Sequence 4910, Application US/10467657
 / Publication No. US2005026051A1
 / GENERAL INFORMATION:

/ APPLICANT: CHIRON SPA

/ APPLICANT: FONTANA Maria Rita

/ APPLICANT: PIZZA Mariagrazia

/ APPLICANT: MASIGNANI Vega

/ APPLICANT: MONACI Elisabetta

/ TITLE OF INVENTION: GONOCOCAL PROTEINS AND NUCLEIC ACIDS
 / FILE REFERENCE:
 / CURRENT APPLICATION NUMBER: US/10/467,657/ PRIOR FILING DATE: 2003-08-11
 / PRIOR APPLICATION NUMBER: GB-0103424-8
 / PRIOR FILING DATE: 2001-02-12
 / NUMBER OF SEQ ID NOS: 9218
 / SOFTWARE: Seqwin99, version 1.04
 / SEQ ID NO: 4910
 / LENGTH: 820
 / TYPE: PRT
 / ORGANISM: Neisseria gonorrhoeae

Result No.	Score	Query	Match	Length	DB ID	Description
1	1410	32.6	820	6	US-10-467-657-4910	Sequence 4910, AP
2	1395.5	32.2	804	7	US-11-070-080-18	Sequence 18, App1
3	156	3.6	824	6	US-10-957-569-31	Sequence 29, App1
4	156	3.6	824	7	US-11-097-589-29	Sequence 50, App1
5	153.5	3.5	817	6	US-10-793-626-50	Sequence 54, App1
6	153.5	3.5	817	6	US-10-793-626-50	Sequence 54, App1
7	150.5	3.5	611	6	US-10-434-437-54	Sequence 202, App1
8	150.5	3.5	697	6	US-10-485-517-202	Sequence 50, App1
9	150.5	3.5	925	6	US-10-454-437-50	Sequence 96, App1
10	144.5	3.3	716	6	US-10-131-826A-96	Sequence 4, App1
11	143	3.3	220	7	US-11-040-595-4	Sequence 3168, App1
12	141.5	3.3	769	6	US-10-467-657-3280	Sequence 20, App1
13	141	3.3	655	6	US-10-467-657-3168	Sequence 215, App1
14	134.5	3.1	825	7	US-11-074-176-20	Sequence 1401, App1
15	134	3.1	389	6	US-10-821-23-1401	Sequence 3, App1
16	133.5	3.1	1786	7	US-11-196-400-3	Sequence 40, App1
17	132	3.0	350	6	US-10-454-437-40	Sequence 158, App1
18	131	3.0	709	7	US-11-047-176-158	Sequence 214, App1
19	129.5	3.0	2665	7	US-11-124-368A-214	Sequence 215, App1
20	129.5	3.0	2668	7	US-11-124-368A-215	Sequence 6084, App1
21	127.5	2.9	859	6	US-10-467-657-6084	Sequence 307, App1
22	126.5	2.9	459	6	US-10-485-51-307	Sequence 3092, App1
23	125.5	2.9	440	6	US-10-661-23-1330	Sequence 1330, App1
24	124.5	2.9	1960	7	US-11-069-834-48	Sequence 48, App1

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THE ECONOMICS OF THE FEDERAL BUDGET 101

run on: February 4, 2006, 13:56:40 ; Search time 50 Seconds
(without alignments)
1408.794 Million cell updates/sec

卷之三

perfect score: 4331

Digitized by srujanika@gmail.com

Scoring table: BLOSUM62

卷之三

searched: 5/2060 seqbs, 826/3659 residues

total number of hits satisfying chosen parameters:

length: 8

maximum B3 seq length: 2888888888

Post-processing: Minimum Match 81

MAXIMUM MATCH 100%

1. Database : ISSUED PATENTS AND PENDING PATENT APPLICATIONS

2: /cgn2_6/prodata/1/iaa/6_COMB.pep:*

PTTUS COMB. den: *

5: /cgn2_6/ptodata/1/ias/bachpep.*
 6: /cgn2_6/ptodata/1/ias/bachpep.*

Result No.	Score	Query Match	Length	DB ID	Description
		No.			
1	4331	100.0	852	2	US-09-741-150-2
2	4331	100.0	852	2	US-10-160-187-2
3	1869.5	43.2	884	2	US-09-141-150-4
4	1869.5	43.2	884	2	US-10-160-187-4
5	1745.5	40.3	810	2	US-09-902-560-11337
6	1407.5	32.5	820	2	US-09-252-91A-30204
7	1406.5	32.5	832	2	US-09-540-306-3056
8	1396.5	32.2	790	2	US-09-543-681A-6859
9	1390.5	32.1	822	2	US-09-328-952-5754
10	1378	31.8	845	2	US-09-489-039A-13590
11	1284	29.6	809	2	US-09-252-991A-29280
12	1251	28.9	937	1	US-08-253-15A-31
13	1251	28.9	937	2	US-09-338-032-1092
14	1251	28.9	937	2	US-09-949-002-374
15	1250	28.9	959	2	US-09-538-002-1091
16	1224	28.3	825	2	US-09-438-185B-29
17	1123	25.9	838	2	US-09-247-796A-17648
18	976	22.5	783	2	US-09-248-796A-16773
19	886	20.5	440	2	US-09-198-452B-44
20	407	9.4	562	2	US-09-949-002-426
21	390	9.0	458	2	US-09-770-796A-146541
22	353	8.2	157	2	US-09-861-451A-8
23	316	7.8	424	2	US-09-198-452A-45
24	327	7.6	191	2	US-09-270-796A-6233
25	165	3.8	3433	2	US-09-091-501B-10
26	165	3.8	3433	2	US-09-538-002-1136
27			900	2	US-09-248-796A-16848

228	161	3.7	761	2	US-09-3228-352-7992	Sequence 7492, AP
229	159	3.7	701	2	US-09-134-001C-3327	Sequence 3327, AP
330	156.5	3.6	767	2	US-09-252-991A-31198	Sequence 31198, AP
331	153.5	3.5	817	2	US-09-710-279-50	Sequence 50, APP1
332	153.5	3.5	817	2	US-09-710-279-1528	Sequence 1528, AP
333	153.5	3.5	823	2	US-09-134-001C-0081	Sequence 4081, AP
334	153.5	3.5	863	2	US-09-3228-352-6730	Sequence 6730, AP
335	152.5	3.5	726	2	US-09-252-991A-26767	Sequence 26767, A
336	152	3.5	422	2	US-09-134-001C-3034	Sequence 3034, AP
337	151	3.5	335	2	US-09-134-000C-0044	Sequence 4044, AP
338	150.5	3.5	611	2	US-09-602-777A-54	Sequence 54, APP1
339	150.5	3.5	697	2	US-09-816-177-2	Sequence 2, APP11
440	150.5	3.5	925	2	US-09-602-777A-50	Sequence 50, APP1
441	150	3.4	724	2	US-09-489-039A-12100	Sequence 12100, A
442	146.5	3.4	556	2	US-09-134-000C-3848	Sequence 3848, AP
443	146	3.4	903	2	US-09-328-352-6479	Sequence 6479, AP
444	145.5	3.4	689	2	US-09-134-000C-4499	Sequence 4499, AP
445	145	3.3	546	2	US-09-489-039A-9627	Sequence 9627, AP

ALIGNMENTS

RESULT 1
US-09-741-150-2
Sequence 2, Application US/09741150
Patent No. 6436689
GENERAL INFORMATION:
APPLICANT: GUTECHER, Karl et al.
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEAR ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO00968
CURRENT APPLICATION NUMBER: US/09/741,150
CURRENT PUBLISH DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 652
TYPE: PRT
ORGANISM: Human
US-09-741-150-2

Query Match	Match	Score 4331;	DB 2;	Length 852;
Best Local Similarity	Similarity	100.0%;	Pred. No. 0;	
Matches	Conservative	100.0%;	Mismatches. 0;	Indels 0;
1	MSSVSIQPSRLPILLTHEGVLPGSTMRSDAHLNOLYRSRLLKGTSQ			
1	MSSVSIQPSRLPILLTHEGVLPGSTMRSDAHLNOLYRSRLLKGTSQ			
61	PNTPDBASDAQLPPHRIGTAALAVQVYGSNNWPKPHYLITLGCRFQIVQV			
61	PNTPDBASDAQLPPHRIGTAALAVQVYGSNNWPKPHYLITLGCRFQIVQV			
121	IAYBOLDLREBPNTCKMRBELLGELSBOPKYKAQLVLEMIDMSPVAVAKLRR			
121	IAYBOLDLREBPNTCKMRBELLGELSBOPKYKAQLVLEMIDMSPVAVAKLRR			
181	EALPDILTSIRTSNKEKLQLDAYSLEERFKMTIPLLVRQEGLLQLQTRK			
181	EALPDILTSIRTSNKEKLQLDAYSLEERFKMTIPLLVRQEGLLQLQTRK			
241	RVIAIRPIRRTHTISCTLEDDEDDEDNDIYMLKEKIRTSMPPEQAHKCVKE			
241	RVIAIRPIRRTHTISCTLEDDEDDEDNDIYMLKEKIRTSMPPEQAHKCVKE			
301	PQSMEYALTRNYLLEMVELPWNKSTTDRDIRARILLDNDHYAMEKLKERV			
301	PQSMEYALTRNYLLEMVELPWNKSTTDRDIRARILLDNDHYAMEKLKERV			
361	QLKNNIKGPILCPVGPGVKTSVGRSVAKTLGRPFHIALGGCDQSDFRH			

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OM protein - protein search, using sw model

Run on: February 4, 2006, 13:48:40 ; Search time 259 Seconds
(without alignments)

2320.888 Million cell updates/sec

Title: US-10-612-012-2

Perfect score: 4331

Sequence: MSSVSPQIPIPSRPLLTHE.....AAFDGGFTVKTRPGLLNSKL 852

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:

2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05-80:
1: uniprot_sprot:
2: uniprot_trembl:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	4323	99.8	852	2	086WA8_HUMAN		086wa8 homo sapien
2	4319	99.7	852	2	08NCB9_HUMAN		08ncb9 homo sapien
3	4292	99.1	852	2	05R6M5_PONPY		05r6m5 pongo pygmaeus
4	4154	95.9	852	2	09DBN5_MOUSE		09dbn5 mus musculus
5	3629	63.8	715	2	08N3B9_HUMAN		08n3b9 homo sapien
6	3376	77.9	840	2	05POY6_BRARE		05poy6 brachydanius
7	2972	68.6	581	2	096K4J_HUMAN		096k4j homo sapien
8	2863	66.1	806	2	08TX13_RAT		08tx13 rattus norvegicus
9	2089	48.2	432	2	08BBK80_MOUSE		08bbk80 mus musculus
10	1890.5	43.7	874	2	04T681_TETNG		04t681 tetrodon nigriventer
11	1869.5	43.2	885	1	1DNH1_MAIZ3		1dnh1 zea mays (mexican corn)
12	1861	43.0	884	2	094F60_9POAL		094f60 dichanthelium
13	1850	42.7	886	2	06RS97_WHATEAT		06rs97 triticum aestivum
14	1849	42.7	888	1	1DNH1_ARATH		064948 arabidopsis thaliana
15	1846.5	42.6	884	2	08GV57_ORYSA		08gv57 orzyza sativa
16	1812.5	41.8	880	2	069SH2_ORYSA		069sh2 orzyza sativa
17	1801	41.6	875	1	1DNH1_SPIOL		004939 spinacia olitoria
18	1784	41.2	843	2	04NPW6_9DSET		04npw6 anaeromyxobacter
19	1745.5	40.3	826	1	1DNQ2_MTXKA		036774 myxococcus xanthus
20	1596	36.9	819	2	0747S2_GEOSEL		0747s2 geobacter sphaericus
21	1585.5	36.6	788	2	082V32_NITRU		082v32 nitrosoforma
22	1573	36.3	775	2	05KWK1_GEORGA		05kwk1 geobacillus
23	1564	36.0	774	2	05KGJ6_BACUL		065916 bacillus
24	1559.5	36.0	776	2	081704_BACCR		081704 bacillus cereus
25	1546.5	35.7	796	2	089H21_BRAGAN		089h21 bradyrhizobium
26	1545.5	35.7	776	2	06HSS4_BACIN		06hs84 bacillus anatum
27	1545	35.7	557	2	08GT60_ARATH		08gt60 arabidopsis thaliana
28	1544.5	35.7	776	2	0633X4_BACCA		0633x4 bacillus
29	1543.5	35.6	773	2	081LC1_BACAN		081lc1 bacillus anatum
30	1541.5	35.6	776	2	06HD56_BACIK		06hd56 bacillus thuringiensis
31	1540	35.6	856	2	Q72C02_DESYH		Q72c02 desulfovibrio

32 1535.5 35.5 773 2 Q4MS75_BACCE
33 1535.5 35.5 773 2 Q72ZV6_BACCI
34 1535 35.4 772 2 Q8CXB9_OCBTH
35 1525.5 35.2 774 2 Q9KBF6_BACDH
36 1525 35.2 783 2 Q7WMZ2_BORER
37 1525 35.2 783 2 Q7MBH0_BORRA
38 1509 34.8 778 2 Q8RC23_THERMOAER
39 1506 34.8 779 1 LON_BRECH
40 1498 34.6 775 2 Q5WEPL_BACSK
41 1497 34.6 774 1 LONI_BACSU
42 1493 34.5 779 2 Q84FG5_BREVIBACIL
43 1482 34.2 768 2 Q74EN9_GEOSEL
44 1477.5 34.1 932 2 Q4WD9_ASPPU
45 1476.5 34.1 937 2 Q7SA85_NEUCCR

ALIGNMENTS

RESULT 1 HUMAN
Q86WA8_HUMAN PRELIMINARY;
ID Q86WA8_HUMAN PRELIMINARY;
AC Q86WA8_HUMAN PRELIMINARY;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Peroxidase; Ion protease.
GN Name=LONG;
OS Homo sapiens (Human).
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo sapiens (Human).
NCBI_TaxID=9606;
RN [1] _
RN NUCLEOTIDE_SEQUENCE.
RN De Wallque S., Van Veldhoven P.P.;
RN Submitted (PEB-2003) to the EMBL/GenBank/DDBJ databases.
RN [2]
RN NUCLEOTIDE_SEQUENCE.
RN TISSUE=Brain;
RN MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RN Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RN Klausner R.D., Collins P.S., Schuler G.D.,
RN Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.M., Bhat N.K.,
RN Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RN Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RN Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RN Brownstein M.J., Usdin T.B., Yoshiyuki S., Carninci P., Prange C.,
RN Raha S.S., Loquelandano N.A., Peters J., Abramson R.D., Mullany S.J.,
RN Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RN Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RN Villalona D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RN Falney J., Heitton E., Kettenbach A., Madan A., Rodriguez S., Sanchez A.,
RN Blakesley R.N., Touchman J.W., Green B.D., Bouffard G.G.,
RN Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RN Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
RN Scherzer A., Schein J.B., Jones S.J.M., Marra M.A.;
RN "Generation and initial analysis of more than 15,000 full-length human
RN and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]

RN NUCLEOTIDE_SEQUENCE.
RN TISSUE=Brain;
RN NIH MGIC Project;
RN Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
RN EMBL; AU548761; CAD68387.1; -; mRNA.
RN DR; BC093912; AAH93912.1; -; mRNA.
RN DR; BC093910; AAH93910.1; -; mRNA.
RN DR; HSP87; P08177; -; mRNA.
RN DR; M89OP5; S16_006; -;
RN DR; Ensembl; ENSEMBL00000102910; Homo sapiens.
RN GO; GO:0005524; P:ATP binding; IBA.

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OM protein - protein search, using bw mode

Run on: February 4, 2006, 13:52:15 ; Search time 48 Seconds

Title: US-10-612-012-2 (without alignments)
Perfect score: 4331
Sequence: 1 MSSVSPQIPLRLLTBE.....AAPDGGFTVTRPGLLNSKL 852

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80;*

1: Pir1;*

2: Pir2;*

3: Pir3;*

4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	189.5		43.2	885	1	T04321	endopeptidase La h
2	180.1		41.6	875	2	T09142	endopeptidase La h
3	1745.5		40.3	827	1	A36895	endopeptidase La h
4	1520.5		35.2	774	2	BB4031	ATP-dependent prot
5	1506.6		34.8	779	1	BA42375	endopeptidase La h
6	1497.7		34.6	774	1	BA42421	endopeptidase La h
7	1474.5		34.0	817	1	A48844	ATP-dependent prot
8	1467.7		33.9	821	2	B75530	ATP-dependent prot
9	1453.5		33.6	813	2	G75331	endopeptidase La h
10	1450.5		33.4	787	2	A70230	probable endopeptidase La h
11	1433.3		33.1	820	2	H81908	ATP-dependent prot
12	1426.6		32.9	820	2	H81106	Lon protease PA1
13	1406.5		32.5	798	2	G83420	ATP-dependent prot
14	1403.5		32.4	786	2	GB2141	ATP-dependent prot
15	1400.5		32.3	799	2	C87492	endopeptidase La h
16	1398.7		32.3	795	1	A70322	ATP-dependent Lon protease [Impo]
17	1393.5		31.7	782	2	B97224	endopeptidase La h
18	1372.5		31.7	784	2	AB0558	endopeptidase La h
19	1371.2		31.7	823	2	AF3361	endopeptidase La h
20	1371.5		31.7	779	2	B97778	ATP-dependent prot
21	1365.5		31.6	805	2	AH2731	ATP-dependent prot
22	1369.5		31.6	805	2	G97512	ATP-dependent seri
23	1368.8		31.6	848	2	C82212	endopeptidase La h
24	1367.5		31.6	784	1	SUECLA	hypothetical prote
25	1367.7		31.6	810	1	JC5045	endopeptidase La h
26	1365.5		31.5	784	1	A71704	endopeptidase La h
27	1364.5		31.5	803	1	A61070	endopeptidase La h
28	1362.5		31.5	784	2	E90690	hypothetical prote
29	1358.8		31.4	799	2	A85541	hypothetical prote

RESULT 1

T04321

endopeptidase La homolog (EC 3.4.21.-) LON1 precursor, mitochondrial - maize

N;Alternate names: ATP-dependent proteinase LON1; ATP-dependent serine proteinase La homolog

N;Contains: adenosinetriphosphatase (EC 3.6.1.3)

C;Species: Zea mays (maize)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T04321

R;Barakat, S.; Pearce, D.A.; Sherman, F.; Rapp, W.D.

Plant Mol. Biol. 37, 141-154, 1998

A;Title: Maize contains a Lon protease gene that can partially complement a yeast pim1-1

A;Reference number: Z15282; PMID:98281532; PMID:9620272

A;Accession: T04321

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-885 <BAR>

A;Cross-references: UNIPROT:P03647; UNIPARC:UP1000043401; EMBL:U85494; NID:91816585; P:

C;Genetics:

A;Gene: LON2

C;Function:

A;Description: serine proteinase

C;Superfamily: ATP-dependent Lon protease

C;Keywords: ATP; DNA binding; hydrolase; mitochondrial matrix; nucleotide-binding motif A (P-1-loop)

F;409-416;Region: nucleotide-binding motif A (P-1-loop)

F;472-477;Region: nucleotide-binding motif B

F;781;Active site: Ser #status predicted

Query Match 43.2%; Score 1869.5; DB 1; Length 885;

Best Local Similarity 44.1%; Pred. No. 3.1e-88;

Matches 401; Conservative 161; Mismatches 269; Indels 67; Gaps 15;

Qy 3 SVSPIQPSRLPLLIPLHEGVLPGLGSTMRTSYDSAHNLQLVRSRLLKGTSLSOTLQVLP- 61

Db 2 SDSPVPLSPRLAVLPFRNKVLPLGAIVRKCTNPSSVQLVEQELWQ-KEBKGLIGVLPV 59

Qy 62 -----NTPDASDA-----QDL----PP-----PQL-----QDL----PP-----HRIGTAAAVQV 88

Db 60 RDSEATAVGSSLSPGSDSPEGSVKGGSAEVSSQDNTKTEQEQPDLI 118

Qy 89 VGSNWPKPH---YILLITGICRFQIVQVLKEKPYIAEVQDRLBEPPTCKMRREBELG 144

Db 119 LSRGVEKPSGRVTVLGLCRPSYELSARGPYHARYSRDLMTKTEQEQPDLI 178

Qy 145 BLSSQPKYAVQLVENDMSPVAVAKLRLLSDPPEALDILTSIRTSNEKEQQLIDA 204

Db 179 ALSRQPKATAMELISLEQOKTVGRTKVLDLTVPYRLADIFVASPBISFBOLSMQLDS 238

Qy 205 VSLERFFKMTPLLYRQIEGH----KLLQTKRKPKQDDDRKVIAPRIRRTHISCTLBD 260

Db 239 VHLKVRISLSKATEBLVQDHLSQSKSQFPLRQMAKTEBKG---- 294

Qy 261 EDEDEDDNDIIVMLEKKIRTSSMMPQAHKVCVKEIKLKKNPQSMPBYALTRNYLEMLVEL 320

ALIGNMENTS

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using SW model

Run on: February 4, 2006, 13:48:20 ; Search time 200 Seconds
(without alignments)
18.71.754 Million cell updates/sec

Title: US-10-612-012-2

Perfect score: 4331

Sequence: 1 MSSVSPIQPSRLPLLLTHE.....AAFPGGFTVKTRPGLLNSKL 852

Scoring table: BLOSUM62

Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseqp_21:*

1: Geneseqp1980s:*

2: Geneseqp1980s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003a:*

7: Geneseqp2003b:*

8: Geneseqp2004s:*

9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	4331	100.0	852 5 ABG32363	Abg32363 Human ATP
2	4331	100.0	852 7 ADM56266	Adm56266 Human ATP
3	4331	100.0	852 9 ADV85873	Adv85873 Human pro
4	4323	99.8	852 4 AAB47562	Aab47562 Protease
5	4323	99.8	852 7 ADC10040	Adc10040 Human NOV
6	4319	99.7	852 4 Aam93785	Aam93785 Human pol
7	4319	99.7	852 8 ADI31771	Adi31771 Human pro
8	4316	99.7	852 5 ABP69443	Abp69443 Human pol
9	3520	81.3	693 7 ADJ70423	Adj70423 Human he
10	2972	68.6	581 4 AAB95332	Aab95332 Human pro
11	2972	68.5	581 4 AAB99179	Aab99179 Human ATP
12	2957	68.3	581 8 ADR08963	Adr08963 Human pro
13	2921	67.4	571 4 AAB94288	Aab94288 Human pro
14	2201	50.8	432 4 AAB97167	Aab97167 Human ATP
15	2201	50.8	432 4 AAB11085	Aab11085 Human ATP
16	2165	50.0	433 6 ABU1611	Abu1611 Human MDD
17	1983.5	45.8	423 4 AAB17375	Aab17375 Novel sig
18	1983.5	45.8	423 7 ADB94083	Adb94083 Human nov
19	1974	45.6	391 5 ABB89248	Abb89248 Human pol
20	1869.5	43.2	884 7 ADM56268	Adm56268 Human ATP
21	1869.5	43.2	884 9 ADV85875	Adv85875 Zea mays
22	1849	42.7	888 8 ADN74069	Adn74069 Thale cre
23	1840.5	42.5	887 8 ADT60761	Adt60761 Plant pol
24	1745.5	40.3	9 ABM92138	Abm92138 M. xanthu

Homo sapiens.

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OS

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20000US-0252410P.

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21-DEC-2000;

20000US-00741150.

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22-NOV-2000;

20000US-0252410P.

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27-JUN-2002.

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PR

21-DEC-2000;

20000US-00741150.

Gencore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Om protein - protein search, using bw model

Run on: February 4, 2006, 13:57:10 : Search time 177 Seconds
(without alignments)
2011.246 Million cell updates/sec

Title: US-10-612-012-2

Perfect score: 4331

Sequence: 1 MSSVSPQIOPSRPLLLTHE.....AAFDGGETVKTRPGLLNSKL 852

Scoring table: BL0S0M62

Gapext 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing First 45 summaries

Database : Published_Applications_AA_Main:
1: /cgn2_6/_ptodata/1/pubaa/US07_PUBCOMB.pep:
2: /cgn2_6/_ptodata/1/pubaa/US08_PUBCOMB.pep:
3: /cgn2_6/_ptodata/1/pubaa/US09_PUBCOMB.pep:
4: /cgn2_6/_ptodata/1/pubaa/US10A_PUBCOMB.pep:
5: /cgn2_6/_ptodata/1/pubaa/US10B_PUBCOMB.pep:
6: /cgn2_6/_ptodata/1/pubaa/US11_PUBCOMB.pep:
* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Summaries

Result No.	Score	Query Match	Length	DB ID	Description
1	4331	100.0	852	3 US-09-711-150-2	Sequence 2, Appli
2	4331	100.0	852	5 US-10-612-012-2	Sequence 2, Appli
3	4333	99.8	852	5 US-10-231-032-4	Sequence 4, Appli
4	3520	81.3	693	4 US-10-408-0765-2229	Sequence 2229, Appli
5	2201	50.8	432	4 US-10-156-239-44	Sequence 44, Appli
6	1933.5	45.8	423	3 US-09-764-868-940	Sequence 940, Appli
7	1974	45.6	391	4 US-10-264-237-1624	Sequence 1624, Appli
8	1869.5	43.2	884	3 US-09-741-150-4	Sequence 4, Appli
9	1869.5	43.2	884	5 US-10-612-012-2	Sequence 4, Appli
10	1869.5	43.2	885	4 US-10-156-239-47	Sequence 47, Appli
11	1840.5	42.5	887	5 US-10-739-910-10838	Sequence 1038, Appli
12	1745.5	40.3	827	4 US-10-363-493-9794	Sequence 19432, Appli
13	1657.5	38.3	850	4 US-10-431-963-156016	Sequence 156016,
14	1585.5	36.6	770	4 US-10-369-493-19725	Sequence 19725, Appli
15	1557.5	36.0	769	4 US-10-363-493-16622	Sequence 16622, Appli
16	1546.5	35.7	794	4 US-10-282-122-45766	Sequence 45766, Appli
17	150.5	35.6	767	4 US-10-363-493-9794	Sequence 9794, Appli
18	154.5	35.6	786	4 US-10-363-493-8915	Sequence 8915, Appli
19	1557.5	35.2	774	4 US-10-369-493-17386	Sequence 17386, Appli
20	1522	35.1	624	4 US-10-767-701-144549	Sequence 44549, Appli
21	1470.5	34.6	774	4 US-10-363-493-23224	Sequence 23224, Appli
22	1470.5	34.0	817	4 US-10-363-493-19217	Sequence 19217, Appli
23	1468.5	33.9	771	4 US-10-369-493-10398	Sequence 10398, Appli
24	1461	33.9	821	4 US-10-363-493-2416	Sequence 23416, Appli
25	1461	33.7	777	4 US-10-363-493-9140	Sequence 9140, Appli
26	1453.5	33.6	813	4 US-10-369-493-645	Sequence 645, Appli
27	1450	33.5	788	4 US-10-369-493-11178	Sequence 11178, Appli

Alignments

RESULT 1
US-09-741-150-2
; Sequence 2, Application US/09741150
; Publication No. US20020081704A1
; GENERAL INFORMATION:
; APPLICANT: GURGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: C1000368
; CURRENT APPLICATION NUMBER: US/09/741,150
; CURRENT FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SBO ID NO: 2
; LENGTH: 852
; TYPE: PRT
; ORGANISM: Human
US-09-741-150-2

Query Match 100.0% ; Score 4331; DB 3; Length 852;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MSSVSPQIOPSRPLLLTHEGYLPPOSTMRSPDSAHNQLVRSRLLKGTSLQSTLGVI 60
DB 1 MSSVSPQIOPSRPLLLTHEGYLPPOSTMRSPDSAHNQLVRSRLLKGTSLQSTLGVI 60

Query 61 PNTPDPASDAQDPLPRLHRIGTAALAVVVGSNWPKPHYLITGLCRFOIVVQLKRPYP 120
DB 61 PNTPDPASDAQDPLPRLHRIGTAALAVVVGSNWPKPHYLITGLCRFOIVVQLKRPYP 120

Query 121 IAEVEQDLRLEBFPTNCMRREBLGILSBOFYKXAVOLVEMILDMSPVAVAKLGRLLDSLPR 180
DB 121 IAEEQDLRLEBFPTNCMRREBLGILSBOFYKXAVOLVEMILDMSPVAVAKLGRLLDSLPR 180

Query 181 EALPDILTSIRTSNKEKLQLDAYSLEERFMTPLVYRQEGLKLQKTPRKPKQDDDK 240
DB 181 EALPDILTSIRTSNKEKLQLDAYSLEERFMTPLVYRQEGLKLQKTPRKPKQDDDK 240

Query 181 POSMPPEALTYNLBLMELVPLWNKSTTDRDQRAIRLLDNDHYAMEKLKERVLEYLA VR 360
DB 181 POSMPPEALTYNLBLMELVPLWNKSTTDRDQRAIRLLDNDHYAMEKLKERVLEYLA VR 360

Query 241 RVIAIRPIRIRTHISGTLDEDBDDEDDBDLIVLWLEKCLRTSSMPHQAHKVCGVBIKRKXW 300
DB 241 RVIAIRPIRIRTHISGTLDEDBDDEDDBDLIVLWLEKCLRTSSMPHQAHKVCGVBIKRKXW 300

Query 361 QLKONTKGPILCFGPGVGKTSVGRGSVAKTIGREFHRIALGGVCQDSDTRGHRRRTVGS 420